



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/784,553B
Source: OIPB
Date Processed by STIC: 4-17-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
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U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Revised 01/29/2002

Does Not Comply
Corrected Diskette Needed



OIPF

RAW SEQUENCE LISTING

DATE: 04/17/2003

PATENT APPLICATION: US/09/784,553B

TIME: 09:27:41

Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

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2 <110> APPLICANT: Zhou, Ming-Ming
3   Aggarwal, Aneel
5 <120> TITLE OF INVENTION: Methods of Identifying Modulators of Bromodomains
7 <130> FILE REFERENCE: 2459-1-003CIP
9 <140> CURRENT APPLICATION NUMBER: 09/784,553B
10 <141> CURRENT FILING DATE: 2001-02-16
12 <150> PRIOR APPLICATION NUMBER: 09/510,314
13 <151> PRIOR FILING DATE: 2000-02-22
15 <160> NUMBER OF SEQ ID NOS: 60
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3014
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <400> SEQUENCE: 1
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28 cagggcgcgg agcagagtcc cgggcaggag aaccaagga gggcgtgtgc tgtggcggcg      180
29 gcggcagcgg cagcggagcc gctagtcccc tccctcctgg gggagcagct gccgccgctg      240
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31 cgctaggggg agggcggggg cggggagggg ggtgggcgaa gggggcgga gggcgtgggg      360
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33 cctgacactc ggcgcctcct gccgtgctcc ggggcggcat gtccgaggct ggcggggccg      480
34 ggccggggcg ctgcggggca ggagccgggg caggggccgg gcccgggggc ctgccccgcg      540
35 agcctgcggc gcttccgccc gcgccccgcg agggctcccc ctgcgccgct gccgccgggg      600
36 gctcggggcg ctgcgggtcc gcgacggcag tggctgcagc gggcacggcc gaaggaccgg      660
37 gaggcggtgg ctcgcccca atcgccgtga agaaagcgca actacgctcc gtcgccgggg      720
38 ccaagaaact ggagaaactc ggagtgtact ccgcctgcaa ggccgaggag tcttgtaaat      780
39 gtaatggctg gaaaaaccct aaccctcac ccaactcccc cagagccgac ctgcagcaaa      840
40 taattgtcag tctaacagaa tcctgtcgga gttgtagcca tgccctagct gctcatgttt      900
41 cccacctgga gaatgtgtca gaggaagaaa tgaacagact cctgggaata gtattggatg      960
42 tggaatatct ctttacctgt gtccacaagg aagaagatgc agataccaaa caagttttatt      1020
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44 gctctttgga aaagaaaccc ccatttgaaa aacctagcat tgaacagggt gtgaataact      1140
45 ttgtgcagta caaatttagt cacctgccag caaaagaaag gcaaacaata gttgagttgg      1200
46 caaaaatggt cctaaaccgc atcaactatt ggcattctgga ggcaccatct caacgaagac      1260
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49 ggagaacatt gcttcgctcg gtcttctact ttatgaggcg acaactcctg gaacaagcaa      1440
50 gacaggaaaa agataaactg cctcttgaaa aacgaactct aatcctcact catttcccaa      1500
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52 attttctctc agcctcttcc agaaccagcc agctaggcat ccaaacagtt atcaatccac      1620
53 ctctgtggc tgggacaatt tcatacaatt caacctcatc ttcccttgag cagccaaacg      1680

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54 cagggagcag cagtcctgcc tgcaaagcct cttctggact tgaggcaaac ccaggagaaa 1740
55 agaggaaaat gactgattct catgttctgg aggaggccaa gaaaccccga gttatggggg 1800
56 atattccgat ggaattaatc aacgagggtta tgtctaccat cacggaccct gcagcaatgc 1860
57 ttggaccaga gaccaatttt ctgtcagcac actcggccag ggatgaggcg gcaagggttg 1920
58 aagagcgagc ggggtgtaatt gaatttcacg tggttggcaa ttccctcaac cagaaaccaa 1980
59 acaagaagat cctgatgtgg ctggttggcc tacagaacgt tttctccac cagctgcccc 2040
60 gaatgcaaaa agaatacatc acacggctcg tctttgacct gaaacacaaa acccttgctt 2100
61 taattaaaga tggcctgtgt attggtggtta tctgtttccg tatgttccca tctcaaggat 2160
62 tcacagagat tgtcttctgt gctgtaacct caaatgagca agtcaagggc tatggaacac 2220
63 acctgatgaa tcatttgaaa gaatatcaca taaagcatga catcctgaac ttctcacat 2280
64 atgcagatga atatgcaatt ggatacttta agaaacaggg tttctccaaa gaaattaaaa 2340
65 tacctaaaac caaatatgtt ggctatatca aggattatga aggagccact ttaatgggat 2400
66 gtgagctaaa tccacggatc ccgtacacag aattttctgt catcattaaa aagcagaagg 2460
67 agataattaa aaaactgatt gaaagaaaac aggcacaaat tcgaaaagtt taccctggac 2520
68 tttcatgttt taaagatgga gttcgacaga ttcctataga aagcattcct ggaattagag 2580
69 agacaggctg gaaaccgagt ggaaaagaga aaagtaaaga gccagagac cctgaccagc 2640
70 tttacagcac gctcaagagc atcctccagc aggtgaagag ccatcaaagc gcttggccct 2700
71 tcatggaacc tgtgaagaga acagaagctc caggatatta tgaagttata aggttcccca 2760
72 tggatctgaa aaccatgagt gaacgcctca agaataggta ctacgtgtct aagaaattat 2820
73 tcatggcaga cttacagcga gtctttacca attgcaaaga gtacaacgcc gctgagagt 2880
74 aatactacaa atgtgccaat atcctggaga aattcttctt cagtaaaatt aaggaagctg 2940
75 gattaattga caagtgttt tttttcccc tctgcttctt agaaactcac caagcagtgt 3000
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78 <210> SEQ ID NO: 2

79 <211> LENGTH: 832

80 <212> TYPE: PRT

81 <213> ORGANISM: Homo sapiens

83 <400> SEQUENCE: 2

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85 Met Ser Glu Ala Gly Gly Ala Gly Pro Gly Gly Cys Gly Ala Gly Ala
86 1 5 10 15
88 Gly Ala Gly Ala Gly Pro Gly Ala Leu Pro Pro Gln Pro Ala Ala Leu
89 20 25 30
91 Pro Pro Ala Pro Pro Gln Gly Ser Pro Cys Ala Ala Ala Gly Gly
92 35 40 45
94 Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Gly Thr Ala
95 50 55 60
97 Glu Gly Pro Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala
98 65 70 75 80
100 Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val
101 85 90 95
103 Tyr Ser Ala Cys Lys Ala Glu Glu Ser Cys Lys Cys Asn Gly Trp Lys
104 100 105 110
106 Asn Pro Asn Pro Ser Pro Thr Pro Pro Arg Ala Asp Leu Gln Gln Ile
107 115 120 125
109 Ile Val Ser Leu Thr Glu Ser Cys Arg Ser Cys Ser His Ala Leu Ala
110 130 135 140
112 Ala His Val Ser His Leu Glu Asn Val Ser Glu Glu Glu Met Asn Arg
113 145 150 155 160
115 Leu Leu Gly Ile Val Leu Asp Val Glu Tyr Leu Phe Thr Cys Val His

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116          165          170          175
118 Lys Glu Glu Asp Ala Asp Thr Lys Gln Val Tyr Phe Tyr Leu Phe Lys
119          180          185          190
121 Leu Leu Arg Lys Ser Ile Leu Gln Arg Gly Lys Pro Val Val Glu Gly
122          195          200          205
124 Ser Leu Glu Lys Lys Pro Pro Phe Glu Lys Pro Ser Ile Glu Gln Gly
125          210          215          220
127 Val Asn Asn Phe Val Gln Tyr Lys Phe Ser His Leu Pro Ala Lys Glu
128 225          230          235          240
130 Arg Gln Thr Ile Val Glu Leu Ala Lys Met Phe Leu Asn Arg Ile Asn
131          245          250          255
133 Tyr Trp His Leu Glu Ala Pro Ser Gln Arg Arg Leu Arg Ser Pro Asn
134          260          265          270
136 Asp Asp Ile Ser Gly Tyr Lys Glu Asn Tyr Thr Arg Trp Leu Cys Tyr
137          275          280          285
139 Cys Asn Val Pro Gln Phe Cys Asp Ser Leu Pro Arg Tyr Glu Thr Thr
140          290          295          300
142 Gln Val Phe Gly Arg Thr Leu Leu Arg Ser Val Phe Thr Val Met Arg
143 305          310          315          320
145 Arg Gln Leu Leu Glu Gln Ala Arg Gln Glu Lys Asp Lys Leu Pro Leu
146          325          330          335
148 Glu Lys Arg Thr Leu Ile Leu Thr His Phe Pro Lys Phe Leu Ser Met
149          340          345          350
151 Leu Glu Glu Glu Val Tyr Ser Gln Asn Ser Pro Ile Trp Asp Gln Asp
152          355          360          365
154 Phe Leu Ser Ala Ser Ser Arg Thr Ser Gln Leu Gly Ile Gln Thr Val
155          370          375          380
157 Ile Asn Pro Pro Pro Val Ala Gly Thr Ile Ser Tyr Asn Ser Thr Ser
158 385          390          395          400
160 Ser Ser Leu Glu Gln Pro Asn Ala Gly Ser Ser Ser Pro Ala Cys Lys
161          405          410          415
163 Ala Ser Ser Gly Leu Glu Ala Asn Pro Gly Glu Lys Arg Lys Met Thr
164          420          425          430
166 Asp Ser His Val Leu Glu Glu Ala Lys Lys Pro Arg Val Met Gly Asp
167          435          440          445
169 Ile Pro Met Glu Leu Ile Asn Glu Val Met Ser Thr Ile Thr Asp Pro
170          450          455          460
172 Ala Ala Met Leu Gly Pro Glu Thr Asn Phe Leu Ser Ala His Ser Ala
173 465          470          475          480
175 Arg Asp Glu Ala Ala Arg Leu Glu Glu Arg Arg Gly Val Ile Glu Phe
176          485          490          495
178 His Val Val Gly Asn Ser Leu Asn Gln Lys Pro Asn Lys Lys Ile Leu
179          500          505          510
181 Met Trp Leu Val Gly Leu Gln Asn Val Phe Ser His Gln Leu Pro Arg
182          515          520          525
184 Met Pro Lys Glu Tyr Ile Thr Arg Leu Val Phe Asp Pro Lys His Lys
185          530          535          540
187 Thr Leu Ala Leu Ile Lys Asp Gly Arg Val Ile Gly Gly Ile Cys Phe
188 545          550          555          560

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190 Arg Met Phe Pro Ser Gln Gly Phe Thr Glu Ile Val Phe Cys Ala Val
191                               565                               570                               575
193 Thr Ser Asn Glu Gln Val Lys Gly Tyr Gly Thr His Leu Met Asn His
194                               580                               585                               590
196 Leu Lys Glu Tyr His Ile Lys His Asp Ile Leu Asn Phe Leu Thr Tyr
197                               595                               600                               605
199 Ala Asp Glu Tyr Ala Ile Gly Tyr Phe Lys Lys Gln Gly Phe Ser Lys
200                               610                               615                               620
202 Glu Ile Lys Ile Pro Lys Thr Lys Tyr Val Gly Tyr Ile Lys Asp Tyr
203 625                               630                               635                               640
205 Glu Gly Ala Thr Leu Met Gly Cys Glu Leu Asn Pro Arg Ile Pro Tyr
206                               645                               650                               655
208 Thr Glu Phe Ser Val Ile Ile Lys Lys Gln Lys Glu Ile Ile Lys Lys
209                               660                               665                               670
211 Leu Ile Glu Arg Lys Gln Ala Gln Ile Arg Lys Val Tyr Pro Gly Leu
212                               675                               680                               685
214 Ser Cys Phe Lys Asp Gly Val Arg Gln Ile Pro Ile Glu Ser Ile Pro
215                               690                               695                               700
217 Gly Ile Arg Glu Thr Gly Trp Lys Pro Ser Gly Lys Glu Lys Ser Lys
218 705                               710                               715                               720
220 Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser Ile Leu
221                               725                               730                               735
223 Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu Pro Val
224                               740                               745                               750
226 Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Phe Pro Met
227                               755                               760                               765
229 Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr Val Ser
230                               770                               775                               780
232 Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys
233 785                               790                               795                               800
235 Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu
236                               805                               810                               815
238 Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys
239                               820                               825                               830

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243 <210> SEQ ID NO: 3

244 <211> LENGTH: 16

245 <212> TYPE: PRT

246 <213> ORGANISM: Artificial Sequence

248 <220> FEATURE:

249 <223> OTHER INFORMATION: synthetic bromodomain peptide

251 <220> FEATURE:

W--> 252 <221> NAME/KEY: Xaa

253 <222> LOCATION: (2)..(4)

254 <223> OTHER INFORMATION: Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

256 <220> FEATURE:

W--> 257 <221> NAME/KEY: Xaa

258 <222> LOCATION: (4)..(11)

259 <223> OTHER INFORMATION: Xaa is a maximum of eight amino acids. Each of these can be any amino acid. One, two, or three may be missing.

262 <220> FEATURE:

RAW SEQUENCE LISTING

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TIME: 09:27:41

Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

W--> 263 <221> NAME/KEY: Xaa
 264 <222> LOCATION: (5)..(5)
 265 <223> OTHER INFORMATION: Xaa is a single amino acid that is either Pro, Lys, or His.
 268 <220> FEATURE:

W--> 269 <221> NAME/KEY: Xaa
 270 <222> LOCATION: (6)..(6)
 271 <223> OTHER INFORMATION: Xaa is any single amino acid.
 274 <220> FEATURE:

W--> 275 <221> NAME/KEY: Xaa
 276 <222> LOCATION: (8)..(8)
 277 <223> OTHER INFORMATION: Xaa is a single amino acid that can be either Tyr, Phe, or His.
 280 <220> FEATURE:

W--> 281 <221> NAME/KEY: Xaa
 282 <222> LOCATION: (9)..(13)
 283 <223> OTHER INFORMATION: Xaa is 5 amino acids. Each of these can be any amino acid.
 286 <220> FEATURE:

W--> 287 <221> NAME/KEY: Xaa
 288 <222> LOCATION: (11)..(11)
 289 <223> OTHER INFORMATION: Xaa is a single amino acid that can be either Met, Ile, or Val.
 292 <400> SEQUENCE: 3

W--> 294 Phe Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp
 295 1 5 10 15

298 <210> SEQ ID NO: 4
 299 <211> LENGTH: 12
 300 <212> TYPE: PRT
 301 <213> ORGANISM: Artificial Sequence

W--> 302 <220> FEATURE:
 303 <223> OTHER INFORMATION: synthetic bromodomain peptide

W--> 306 <220> FEATURE:

W--> 307 <221> NAME/KEY: Xaa
 308 <222> LOCATION: (6)..(6)
 309 <223> OTHER INFORMATION: Xaa represents an acetyl-lysine
 311 <400> SEQUENCE: 4

W--> 313 Ile Ser Tyr Gly Arg Xaa Lys Arg Arg Gln Arg Arg
 314 1 5 10

316 <210> SEQ ID NO: 5
 317 <211> LENGTH: 14
 318 <212> TYPE: PRT
 319 <213> ORGANISM: Artificial Sequence
 321 <220> FEATURE:
 322 <223> OTHER INFORMATION: synthetic bromodomain peptide
 325 <220> FEATURE:

W--> 326 <221> NAME/KEY: Xaa
 327 <222> LOCATION: (8)..(8)
 328 <223> OTHER INFORMATION: Xaa represents an acetyl lysine.
 330 <400> SEQUENCE: 5

W--> 332 Ala Arg Lys Ser Thr Gly Gly Xaa Ala Pro Arg Lys Gln Leu
 333 1 5 10

336 <210> SEQ ID NO: 6

All Xaa must be
 accounted for in
 feature

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/784,553B

DATE: 04/17/2003
TIME: 09:27:42

Input Set : A:\2459-1-003 CIP SeqList.txt
Output Set: N:\CRF4\04172003\I784553B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 2,4,5,6,8,9,10,11,12,13,15
Seq#:4; Xaa Pos. 6
Seq#:5; Xaa Pos. 8
Seq#:6; Xaa Pos. 8
Seq#:43; Xaa Pos. 1,2,4,6,7,8,10,11,12,13,14,15,17
Seq#:46; Xaa Pos. 5
Seq#:48; Xaa Pos. 2,4,6,8,10
Seq#:50; Xaa Pos. 5
Seq#:51; Xaa Pos. 5
Seq#:52; Xaa Pos. 5
Seq#:53; Xaa Pos. 5
Seq#:54; Xaa Pos. 5
Seq#:55; Xaa Pos. 5
Seq#:56; Xaa Pos. 5
Seq#:57; Xaa Pos. 6
Seq#:58; Xaa Pos. 7
Seq#:59; Xaa Pos. 16

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 254,259
Seq#:34; Line(s) 1159
Seq#:35; Line(s) 1188
Seq#:43; Line(s) 1448,1453
Seq#:46; Line(s) 1541
Seq#:48; Line(s) 1572,1577,1582,1587

VERIFICATION SUMMARY

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Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

L:252 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:257 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:269 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:275 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:287 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:302 M:283 W: Missing Blank Line separator, <220> field identifier
L:307 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:326 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:346 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:1436 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1441 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1446 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1451 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1456 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1461 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1466 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1471 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1476 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
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L:1539 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:1570 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
L:1575 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
L:1580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
L:1585 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
L:1590 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
L:1596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:1630 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50
L:1636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1648 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51
L:1654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1666 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:52
L:1672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0
L:1684 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:53
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:1702 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:54
L:1708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:1720 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:55
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:1738 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:56
L:1744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:1756 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:57

VERIFICATION SUMMARY

DATE: 04/17/2003

PATENT APPLICATION: US/09/784,553B

TIME: 09:27:42

Input Set : A:\2459-1-003 CIP SeqList.txt

Output Set: N:\CRF4\04172003\I784553B.raw

L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
L:1775 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:58
L:1781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1794 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:59
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0